

## SEQUENCE LISTING

<120> Methods for Protection Against Lethal Infection with Bacill us Anthracis

<130> 22727/04079

<140> 09/747,521.

<141> 2000-12-21

<160> 8

<170> PatentIn version 3.0

<210> 1

<211> 2430

<212> DNA

<213> Bacillus anthracis

<220>

j-d

<221> CDS

<222> (1)..(2430)

<400> 1

atg aat ata aaa gaa ttt ata aaa gta att agt atg tca tgt tta 48

Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu

1

5

10

15

gta aca gca att act ttg agt ggt ccc gtc ttt atc ccc ctt gta cag 96 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln

20 25 30

ggg gcg ggc ggt cat ggt gat gta ggt atg cac gta aaa gag aaa gag 144

Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu

35

40

45



cag gaa gag cat tta aag gaa atc atg aaa cac att gta aaa ata gaa 240
Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu
65 70 75 80

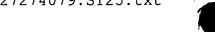
gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca gaa aag cta ctt
288
Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu
85
90
95

gag aaa gta cca tct gat gtt tta gag atg tat aaa gca att gga gga 336
Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly

100 105 . 110

gca tta tct gaa gat aag aaa aaa ata aaa gac att tat ggg aaa gat 432
Ala Leu Ser Glu Asp Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp
130
135
140

gct tta tta cat gaa cat tat gta tat gca aaa gaa gga tat gaa ccc 480 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro 145 150 155 160



gta ctt gta atc caa tct tcg gaa gat tat gta gaa aat act gaa aag 528
Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys

165 170 175

gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att 576
Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile

180 185 190

tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat 624
Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn
195
200
205

acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act 672

Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr

210

215

220

aat cag ctt aag gaa cat ccc aca gac ttt tct gta gaa ttc ttg gaa 720 Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu 225 230 235 240

caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat
768
Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr
245
250
255

tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa 816 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu 260 265 270 gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc 864 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser 275 280 285

ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg
912
Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp
290
295
300

gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa
 960
Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu
305
310
315
320

gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag 1008 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys 325 330 335

aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta 1056 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu 340 345 350

aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa 1104
Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys
355 360 365

gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa 1152 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu

qaa qaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro 390 395 400 385

tta tct gaa aaa gaa aaa gag ttt tta aaa aag ctg aaa ctt gat att 1248 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Leu Lys Leu Asp Ile

405 410 415

caa cca tat gat att aat caa agg ttg caa gat aca gga ggg tta att Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile 420 425 430

gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp 445 440 435

att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg 1392 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu 460 450 455

tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr 470 475 480 465

gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile

485 490 495

aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att 1536 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile

500 505 510

tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat 1584
Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp
515 520 525

aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca 1632 Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala

gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg 1680 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu 545 550 560

gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata 1728 Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile 565 570 575

agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att 1776
Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile
580 585 590

caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg

Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly
595 600 605

tta cca aaa tat aca aag`ctt att aca ttc aac gtg cat aat aga tat 1872
Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr
610 615 620

gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa 1920 Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys 625 630 635 640

aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt 1968
Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val
645
650
655

gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata 2016
Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile
660 665 670

gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca 2064
Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser

aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct
2112
Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro
690
695
700

tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa

Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu

705 710 715 720

ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac

Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn

725 730 735

caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag 2256

Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys

745 740 750

gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa 2304

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu

755 760 765

ttt ttt qca qaa qcc ttt agg tta atg cat tct acg qac cat gct gaa

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu

770 775 780

cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac 2400

Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn

790 795 800 785

gat cag att aag ttc att att aac tca taa 2430

Asp Gln Ile Lys Phe Ile Ile Asn Ser

805



<211> 809

<212> PRT

<213> Bacillus anthracis

<400> 2

Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu 1 5 10 15

Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln 20 25 30

Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu 35 40 45

Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr 50 55 60

Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu 65 70 75 80

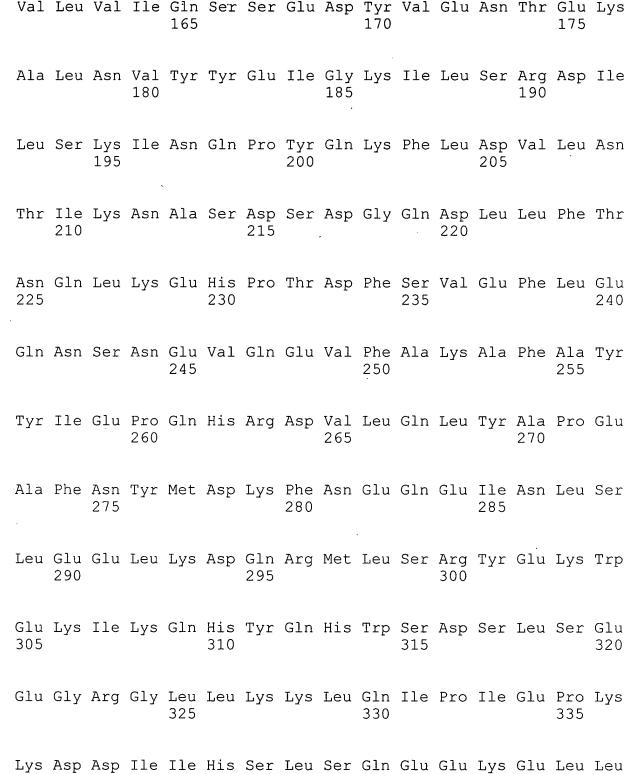
Val' Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu 85 90 95

Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly 100 105 110

Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu 115 120 125

Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp 130 135 140

Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro 145 150 155 160



350

340



Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys 355 360 365

Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu 370 375 380

Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro 385 390 395 400

Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile 405 410 415

Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile 420 425 430

Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp 435 440 445

Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu 450 455 460

Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr 465 470 475 480

Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile 485 490 495

Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile 500 505 510

Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp 515 520 525

Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala 530 535 540



Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu 

Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn 725 730 735

Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys 740 745 750

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu 755 760 765

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu 770 775 780

Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn 785 790 795 800

Asp Gln Ile Lys Phe Ile Ile Asn Ser 805

<210> 3

<211> 2295

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1)..(2295)

<400> 3

atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata 48

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile

1

5

10

15

30

tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa 96 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys

20 25

cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu

txt

35 . . 40 45

cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt 192 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val

50 55 60

acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa 240
Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu

65 70 75 80

aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly

90 95

ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct 336

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala

100 105 110

gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa 384

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys

115 120 125

gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln

130 135 140

ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat 480

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp

145 150 155 160

ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct 528
Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser

165 170 175

agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca 576
Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser
180 185 190

aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac 624
Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp

195
200
205

aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat 672
Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp
210
215
220

gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat
720
Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His
225
230
230
240

gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc 768
Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser

245
250
255

acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att. 816



Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile
260 265 . 270

gat aag aat gta toa ooa gag goa aga oac ooc ott gtg goa got tat 864 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr 275 280 285

ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag
912
Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu
290
295
300

gat caa tcc aca cag aat act gat agt gaa acg aga aca ata agt aaa 960
Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys
305 310 315 320

aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca 1008 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala 325 330 335

gaa gtg cat gcg aat act tct aca agt agg aca cat act agt gaa gta 1056 Glu Val His Ala Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val 340 345 350

cat gga aat gca gaa gtg cat gcg gtc gca att gat cat tca cta tct 1104
His Gly Asn Ala Glu Val His Ala Val Ala Ile Asp His Ser Leu Ser
355 360 365

cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct



1152 . . . Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala
370 375 380

gat aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg 1200 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr 385

gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa 1248
Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys
405
410
415

aat caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa 1296 Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln 420 425 430

ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc 1344

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile

435

440

445

gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat 1392
Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn
450
455
460

tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat 1440
Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp
465
470
475
480

221214019.3123.CXC

acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga 1488

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly

485

490

495

aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg caa 1536
Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln
500 505 510

att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta aat 1584

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn

515

520

525

ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa 1632
Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu
530 535 540

acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt 1680

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe
545

550

560

gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata 1728
Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile
565
570
575

acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag 1776 Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys

Page 18

aat cag tta gcg gaa tta aac gca act aac ata tat act gta tta gat
1824
Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp
595
600
605

aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt 1872
Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg
610 615 620

ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta 1920 Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val 625 630 635 640

gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta 1968 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu 645 650 655

gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga 2064
Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg
675 680 685

tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt 2112

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe
690 695 700

<400>

ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat 2160
Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn
705 710 715 720

ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att 2208
Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile
725 730 735

att aat oot agt gag aat ggg gat act agt acc aac ggg atc aag aaa 2256

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys

740

745

750

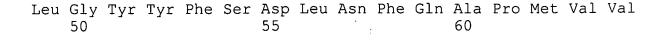
att tta atc ttt tct aaa aaa ggc tat gag ata gga taa 2295
Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly
755
760

<210> 4 <211> 764 <212> PRT <213> Bacillus anthracis

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile 1 5 10 15

Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys 20 25 30

Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Gln Gly Leu 35 40 . 45



Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu 65 70 75 80

Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly 85 90 95

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala 100 105 110

Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys 115 120 125

Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln 130 135 140

Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp145150

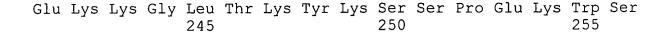
Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser 165 170 175

Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser 180 185 190

Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp 195 200 205

Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp 210 215 220

Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His 225 230 235 · 240



Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile 260 265 270

Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr 275 280 285

Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu 290 295 300

Asp Gln Ser Thr Gln Asn Thr Asp Ser Glu Thr Arg Thr Ile Ser Lys 305 310 315 320

Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala 325 330 335

Glu Val His Ala Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val 340 345 350

His Gly Asn Ala Glu Val His Ala Val Ala Ile Asp His Ser Leu Ser 355 360 365

Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala 370 375 380

Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr 385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys 405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln 420 425 430



Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile 435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn 450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp 465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly
485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln 500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn 515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu 530 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe 545 550 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile 565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys 580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp 595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg 610 615 620



Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val 625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu 645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile 660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg 675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe 690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn 705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile 725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys 740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly 755 760

<210> 5

<211> 19

<212> DNA

<213> synthetic construct

<400> 5

ctgaaaccat cacgtaaaa

19

```
<210>
          6
   <211>
          26
   <212>
          DNA
          synthetic construct
   <213>
   <400>
   agcaagaaat aaatctatag tctaga
   <210>
          7
   <211> 15
   <212> DNA
   <213>
          synthetic construct
   <400> 7
   ctcgagacca tggtt
       15
<210>
          8
   <211> 15
   <212>
          DNA
   <213>
          synthetic construct
   <400> 8
   taaggtaatt ctaga
s
I
       15
Ū
o
```